INTABIOTECH

PROTEOSOL™ · PROPRIETARY PROTEIN-ENGINEERING PLATFORM

Breaking Protein, Building Function

Ultra-Enzymolysis™ as a Platform for Next-Generation Plant Protein Engineering

From controlled proteolysis to highly soluble peptide architectures in ProteoSol™

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Executive perspective

The next generation of plant-protein ingredients will be defined by more than protein percentage or botanical origin. Their industrial value increasingly depends on whether the molecular architecture can be engineered to deliver reproducible solubility, dispersion, optical performance, low sedimentation, acceptable sensory properties and nutritional functionality in demanding food and beverage systems.

Ultra-Enzymolysis™ is INTABIOTECH's proprietary technological platform underlying ProteoSol™. It should not be reduced to the generic statement "enzymatic hydrolysis". The platform is better understood as controlled molecular transformation: the conversion of structurally difficult plant proteins into application-oriented peptide populations whose functional outputs can be measured, standardised and validated.

Abstract

Plant proteins are technologically complex materials. Their behaviour is governed not only by amino-acid composition but also by tertiary and quaternary structure, hydrophobic interactions, disulphide bonding, aggregation state, processing history, pH, ionic strength and interactions with other matrix constituents. Poor aqueous solubility consequently remains one of the major barriers to their use in high-value beverages and functional nutrition. Contemporary literature identifies enzymatic hydrolysis as one of the most powerful approaches for modifying these constraints, while also showing that performance depends on substrate, hydrolysis profile, protein concentration and downstream processing.

Ultra-Enzymolysis™ is INTABIOTECH's proprietary platform for transforming plant-protein structures into lower-molecular-weight peptide systems intended to deliver high water compatibility and application-specific functionality. Operational parameters constitute protected know-how and are excluded from public disclosure; the scientifically relevant outputs, however, can and should be characterised. In ProteoSol™ Rice, controlled documentation reports ≥85% protein on a dry basis, ≥80% peptide content and a molecular-weight distribution in which >80% of peptides are ≤2,000 Da, together with a clear and transparent solution without visible turbidity or sediment under the source preparation conditions.

This review examines the scientific rationale behind Ultra-Enzymolysis™, distinguishes controlled protein engineering from indiscriminate proteolysis, and evaluates its implications for solubility, optical performance, sensory properties, digestive accessibility and advanced beverage formulation.

Keywords: *Ultra-Enzymolysis™; ProteoSol™; plant protein; enzymatic hydrolysis; peptides; protein solubility; molecular-weight distribution; clear protein; rice protein; functional beverages; protein engineering; food technology.*

1. Protein percentage is not protein performance

Protein ingredients are still commonly described through simple compositional variables: 70%, 80% or 90% protein; concentrate or isolate; rice, pea, soy or another source. These descriptors are commercially useful but technologically incomplete. Two ingredients containing the same analytical percentage of protein can behave completely differently once incorporated into water.

One may hydrate rapidly while another forms aggregates. One may remain suspended while another sediments. One may tolerate acidic pH while another precipitates near its isoelectric region. The explanation lies in molecular architecture — size, conformation, charge distribution, hydrophobicity, intermolecular interactions and processing history.

"Protein concentration tells us how much protein exists. It does not tell us how that protein behaves."

2. Why conventional plant proteins are difficult

Many plant proteins evolved biologically as storage proteins, not as beverage ingredients. Their native and process-modified structures are therefore not optimised for instant hydration, transparency or stability in acidic drinks. Hydrophobic domains can promote association; disulphide bridges and hydrogen bonding can stabilise aggregates; drying can impair rehydration; and residual matrix constituents can further influence dispersion and flavour.

The limitations become more severe as the final matrix becomes more demanding. An opaque shake may tolerate particulate material, while a transparent sports drink cannot. A spoonable food may tolerate viscosity, while a protein water cannot. A chocolate system can mask colour and vegetal notes, while a lemon-flavoured clear beverage cannot.

3. Enzymatic hydrolysis: powerful, but not intrinsically sophisticated

Proteolytic enzymes cleave peptide bonds and reduce intact protein structures to smaller polypeptides and peptides. This can alter molecular-weight distribution, surface charge, hydrophobic exposure, solubility, aggregation behaviour, viscosity, sensory profile and susceptibility to gastrointestinal proteolysis.

Experimental work on pea, rice, hemp and oat proteins has demonstrated substantial increases in solubility following controlled enzymatic hydrolysis. The same research also shows an important limitation: higher protein concentration can still favour reassociation and reduce apparent solubility. Hydrolysis therefore increases the probability of success; it does not eliminate the need for concentration- and matrix-specific validation.

SCIENTIFIC DISTINCTION

A protein is not simply “hydrolysed” or “not hydrolysed”. Functional behaviour depends on the molecular population produced by hydrolysis — and on how that population interacts with the final food matrix.

4. Ultra-Enzymolysis™: from hydrolysis to molecular design

This distinction defines the technological territory of Ultra-Enzymolysis™. The platform is not intended as a race towards the highest possible degree of hydrolysis. It is intended to produce application-oriented peptide architectures from structurally difficult plant proteins.

INTABIOTECH’s controlled documentation describes the ProteoSol™ processing concept as enzymatic hydrolysis / gradient cutting of edible plant protein to generate soluble low-molecular-weight peptides. The public scientific narrative should remain focused on this functional logic and on measurable output characteristics, while the operational sequence and enabling conditions remain confidential.

Table 1. Optimisation problem behind Ultra-Enzymolysis™

Engineering objective	Potential benefit	Potential counter-effect
Reduce molecular size	Improved hydration and solubility	Excessive cleavage may increase bitterness
Increase soluble fraction	Reduced macroscopic aggregation and sedimentation	High concentration can still favour reassociation

Engineering objective	Potential benefit	Potential counter-effect
Improve optical performance	Enables clear / low-haze beverage concepts	Colour and nanostructural scattering may remain
Increase digestive accessibility	May facilitate subsequent proteolysis	Does not itself prove superior systemic bioavailability
Lower viscosity	Enables refreshing beverage formats	May alter other interfacial or textural functions
Standardise peptide architecture	Improves reproducibility and technical positioning	Requires validated analytical fingerprinting

5. The central principle: optimum hydrolysis, not maximum hydrolysis

More hydrolysis is not automatically better. Proteolysis exposes peptide sequences that were previously buried inside larger proteins. Some resulting peptides interact favourably with water; others can contribute bitterness or astringency. Recent reviews continue to identify undesirable sensory properties as one of the principal constraints on the use of protein hydrolysates in foods.

The engineering objective is therefore to generate sufficient structural transformation to obtain the required functionality while maintaining acceptable peptide, sensory and nutritional characteristics. This is a multivariable optimisation problem rather than a one-dimensional degree-of-hydrolysis target.

"Maximum hydrolysis is a process endpoint. Optimum hydrolysis is a product-design decision."

6. Molecular-weight distribution as a technological fingerprint

A hydrolysate is not one molecule; it is a population containing residual proteins, polypeptides, medium peptides, oligopeptides and smaller fractions. The distribution between these populations has substantial consequences for functionality. Size-exclusion chromatography is therefore particularly useful because it provides a direct view of the molecular-size architecture of the product.

For ProteoSol™ Rice, current controlled documentation reports that more than 80% of the peptide fraction is ≤2,000 Da. This is technologically significant because it demonstrates a structural state distinct from a conventional intact rice-protein isolate. The next scientific step should be to convert this figure into a validated chromatographic fingerprint with defined method, repeatability, lot-to-lot variability and correlations with solubility, optical performance and sensory behaviour.

7. ProteoSol™ Rice: measurable output of Ultra-Enzymolysis™

ProteoSol™ Rice provides a useful case study because conventional rice protein is particularly challenging from a solubility perspective. The controlled specification defines the ingredient as a rice-protein hydrolysate / rice-peptide ingredient produced from edible rice protein by enzymatic gradient hydrolysis.

Table 2. Current documented output profile — ProteoSol™ Rice

Parameter	Current documented position	Evidence-development action
Protein	≥85.0% dry basis	Confirm method and nitrogen factor in final master specification
Peptide content	≥80.0% dry basis	Define analytical method and lot-release rule
Molecular-weight profile	>80% of peptides ≤2,000 Da	Validate by SEC-HPLC or equivalent; define reproducibility window
Solubility	Instant solubility in source specification	Convert to method-defined soluble-protein recovery at set concentration/pH
Solution appearance	Clear and transparent; no visible turbidity or sediment	Define NTU / % transmittance and sedimentation protocol
Ultra-Clear grade	Development designation	Establish a separate quantitative optical acceptance gate
Amino-acid quality	Pending complete current dataset	Generate aminoacidogram, EAA, limiting amino acid and leucine profile
Digestibility	Comparative superiority not established	Use INFOGEST and, if strategically justified, DIAAS-related evidence

Source: INTABIOTECH / ND Pharma & Biotech controlled ProteoSol™ Rice specification-development dossier, 2026. Product-positioning statements must remain subordinate to approved QA methods and lot documentation.

8. Why solubility changes downstream functionality

Protein solubility is a gateway property. Poor solubility can compromise dispersibility, mouthfeel, sedimentation, optical clarity, processing consistency, flavour perception and the effective protein dose consumed. Improving aqueous compatibility can therefore create benefits far beyond the simple observation that “the powder dissolves”.

Conceptual output chain for Ultra-Enzymolysis™. This is a functional model, not a disclosure of manufacturing sequence or operating parameters.

9. From solubility to optical clarity

Optical clarity is a particularly demanding expression of protein functionality. Light scattering can arise from aggregates, colloidal structures, particles and other discontinuities. Reducing large structures and insoluble fractions can favour

optical performance, but soluble does not automatically mean transparent. A solution may be analytically soluble yet remain opalescent.

For this reason, ProteoSol™ development should continue to separate solubility from optical specification. The current Rice source describes a clear and transparent solution without visible sediment; the Ultra-Clear grade should ultimately be defined by quantitative turbidity and/or transmittance criteria at stated protein concentration, pH, temperature and storage time.

10. Protein concentration is the hidden variable

A protein that looks transparent at 0.5% may behave very differently at 5% or 10%. As concentration increases, molecular proximity, hydration demand, ionic interactions and aggregation equilibria change. Any clear-protein demonstration is therefore incomplete unless it specifies ingredient concentration and actual protein delivered per serving.

APPLICATION RULE

The meaningful question is not “Is ProteoSol™ soluble?” It is “How does this ProteoSol™ reference behave at commercially relevant concentration under the pH, ionic strength, mineral loading, thermal history and shelf-life conditions of the intended product?”

11. Acid, minerals, heat and carbonation: the real stress test

Protein beverages contain far more than protein and water. Organic acids, buffers, sodium, potassium, calcium, magnesium, vitamins, botanical extracts, flavours, sweeteners, colours and preservatives can all change protein behaviour. Divalent minerals can promote bridging interactions; ionic strength can screen electrostatic repulsion; heat can expose hydrophobic regions and induce aggregation; carbonation changes pH, gas-liquid interfaces and foaming behaviour.

A high-value ProteoSol™ reference should therefore be accompanied by an application map rather than a single generic solubility value. Operating windows should be established for pH, protein concentration, mineral load, thermal process and storage conditions relevant to each target category.

12. Hydrolysis and digestive accessibility: mechanism versus claim

Smaller peptides require less proteolytic fragmentation than intact proteins before intestinal absorption as amino acids, dipeptides and tripeptides. It is therefore scientifically reasonable to investigate whether controlled pre-hydrolysis modifies digestion kinetics or digestive accessibility. However, mechanistic plausibility is not the same as demonstrated physiological superiority.

Higher solubility does not automatically prove better systemic bioavailability; smaller peptides do not automatically prove greater muscle-protein synthesis; and rapid digestion does not automatically establish higher protein quality. Protein quality still depends on the indispensable amino-acid profile and digestibility of those amino acids. Until direct evidence exists, Ultra-Enzymolysis™ should be communicated through its molecular and functional outputs rather than unsupported comparative physiological claims.

13. The sensory paradox of peptide technology

Hydrolysis can solve one problem while creating another. As protein structures are cleaved, hydrophobic peptide sequences can become exposed, generating bitterness, astringency or off-notes. A 2026 review in the Journal of Food

Science identified raw-material quality, process conditions and multiple downstream strategies as important determinants of sensory quality in protein hydrolysates.

Sensory science must therefore be integrated into protein engineering. The correct target is neither minimum molecular weight nor maximum degree of hydrolysis, but the peptide-distribution window that delivers required functionality with acceptable taste and mouthfeel.

Table 3. Ultra-Enzymolysis™ design space: what must be optimised together

Domain	Desired output	Analytical / application metric	Why it matters
Molecular	Controlled peptide-size distribution	SEC-HPLC, DH, peptide fingerprint	Defines the structural product rather than a generic hydrolysate
Physicochemical	High aqueous compatibility	Soluble protein recovery, particle size, zeta potential where relevant	Drives dispersion, processing and sedimentation
Optical	Clear / low-haze behaviour	NTU, %T, visual standard	Enables transparent beverage applications
Sensory	Low bitterness / low off-notes	Descriptive sensory, bitterness threshold, aftertaste	Determines consumer acceptability
Process	Robustness under stress	pH, heat, mineral, carbonation and shelf-life challenge	Converts laboratory solubility into industrial performance
Nutrition	Appropriate amino-acid delivery	Aminoacidogram, EAA, leucine, digestibility	Prevents functional engineering from outrunning nutritional quality

14. Ultra-Enzymolysis™ is a platform, not one universal recipe

Different plant proteins present different structural problems. Rice does not behave like pea; pea does not behave like soy; soy does not behave like wheat. Even within the same botanical source, extraction and drying history can materially alter protein behaviour. A technologically sophisticated platform should therefore not assume that one hydrolysis profile is universally optimal.

Ultra-Enzymolysis™ is best conceptualised as a platform architecture capable of adapting the transformation strategy to the characteristics of the starting protein and the functionality required from the finished ingredient. This gives ProteoSol™ the potential to evolve through source-specific and application-specific references rather than as a single generic hydrolysed-protein SKU.

15. What should remain secret

Scientific communication about proprietary process technology must know where to stop. INTABIOTECH's controlled documentation explicitly treats Ultra-Enzymolysis™ as protected trade-secret know-how. Commercial qualification can therefore be based on finished-product identity, safety, quality, reproducibility and performance without transferring enabling manufacturing knowledge.

Table 4. Public evidence versus protected manufacturing know-how

Appropriate for scientific / customer disclosure	Protected Ultra-Enzymolysis™ know-how
• Ingredient identity and source	• Specific enzyme identities or combinations

Appropriate for scientific / customer disclosure	Protected Ultra-Enzymolysis™ know-how
• Approved compositional specification	• Enzyme ratios and dosages
• Molecular-weight distribution	• Operating sequence
• Solubility under defined method	• Reaction times and temperatures
• NTU / transmittance and sedimentation data	• Process pH and control logic
• Sensory performance	• Intermediate treatment conditions
• Application stability	• Proprietary separation / purification strategy
• Safety and regulatory documentation	• Yield optimisation rules
• Batch-to-batch reproducibility	• Termination conditions
• Validated nutritional data	• Any other information enabling reproduction or reverse engineering

IP PRINCIPLE

A technology can be scientifically validated through reproducible outputs without publishing reproducible manufacturing instructions.

16. An output-based evidence model

The strongest scientific strategy for Ultra-Enzymolysis™ is an output-based validation architecture. Each ProteoSol™ reference should be defined by an evidence package spanning molecular, physicochemical, application, sensory and nutritional layers.

MOLECULAR

SEC-HPLC molecular-weight distribution · Degree of hydrolysis · Free amino nitrogen · Peptide fingerprint / residual intact-protein profile

PHYSICOCHEMICAL

Soluble-protein recovery · Turbidity and transmittance · Particle-size distribution · Viscosity / sedimentation

APPLICATION

pH operating window · Mineral tolerance · Thermal and carbonation challenge · Real-time / accelerated stability

SENSORY

Bitterness · Astringency · Vegetal notes · Aftertaste / masking requirements

NUTRITIONAL

Full amino-acid profile · EAA / leucine / limiting amino acid · INFOGEST digestibility · DIAAS-related evidence where justified

17. From process technology to competitive barrier

If each ProteoSol™ reference is associated with a reproducible combination of molecular fingerprint, solubility profile, optical performance, sensory characteristics, processing tolerance and application data, Ultra-Enzymolysis™ ceases to be merely a proprietary process name. It becomes an evidence-backed technology platform.

An ingredient category can often be copied compositionally — for example, a competitor can market a "rice protein hydrolysate". Reproducing the same peptide architecture, clarity, solubility, flavour, stability and processing robustness may be considerably more difficult. The defensible competitive barrier therefore consists of two layers: protected process know-how plus validated application-performance data.

18. Where Ultra-Enzymolysis™ can create the greatest value

The highest-value applications are unlikely to be those in which conventional proteins already perform adequately. The platform becomes most strategically relevant where the matrix imposes difficult conditions or where traditional protein formats carry an unacceptable sensory penalty.

Clear protein waters	Protein delivery without the visual and textural architecture of a milkshake.
Acidic RTD beverages	Fruit-style and refreshing drinks where conventional plant proteins may precipitate or haze.
Hydration + protein	Combining electrolytes and protein while preserving low viscosity and drinkability.
Functional shots	Concentrated functionality in small volume, where sediment or grittiness is unacceptable.
Active nutrition	Pre-, intra- and post-exercise formats beyond conventional shakes.
Healthy ageing / adult nutrition	Lighter protein formats for consumers who reject dense or creamy beverages.
Powder sticks	Rapidly dispersible formats designed for water bottles and on-the-go use.
Selected 0.0 / fermented beverage concepts	Matrices historically difficult to fortify with plant protein without altering appearance or mouthfeel.

19. Scientific programme: recommended next phase

ProteoSol™ already has a meaningful technical foundation. The next objective should be to convert that foundation into a proprietary evidence system. The priority programme should include:

- Validated SEC-HPLC molecular-weight profiling, confirming the ≤2 kDa fraction and lot-to-lot reproducibility.
- Full aminoacidogram including essential amino acids, leucine and limiting amino-acid assessment.
- Standardised soluble-protein recovery across concentration, pH and ionic-strength conditions.
- NTU and optical-transmittance specifications separating Clear from Ultra-Clear.
- Validated degree-of-hydrolysis methodology.
- Accelerated sedimentation and real-time stability programme.
- Sensory peptide mapping focused on bitterness, astringency and flavour compatibility.
- INFOGEST digestion studies combined with peptide-size analysis.
- Benchmark studies against conventional plant protein and relevant clear-whey systems, focused on technological performance.
- Application-specific datasets for protein waters, hydration beverages, acidic RTDs and functional shots.

Conclusion

The future of plant protein will not be decided merely by how much protein can be extracted from a crop. It will increasingly be decided by how precisely that protein can be engineered. Protein structure determines functionality; functionality determines formulation freedom; and formulation freedom determines whether plant protein remains confined to opaque shakes and conventional foods or moves into transparent, refreshing and technologically sophisticated beverages.

Ultra-Enzymolysis™ represents INTABIOTECH's approach to that challenge. Its scientific rationale is not indiscriminate protein destruction. It is controlled molecular transformation. The objective is not maximum hydrolysis, minimum molecular weight or a simplistic claim that "smaller is always better". The objective is an optimal peptide architecture for the intended application.

In ProteoSol™ Rice, the current specification already provides evidence of this approach: high protein content, high peptide content, a predominantly ≤2,000 Da peptide fraction and clear, sediment-free solution behaviour under the stated preparation conditions. The next phase is to connect those outputs quantitatively to optical performance, sensory quality, digestive behaviour and finished-product stability.

"Breaking protein is chemistry. Building function is technology."

ULTRA-ENZYMOLYSIS™ OPERATES AT THE INTERFACE BETWEEN THE TWO.

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Corporate technical note

Ultra-Enzymolysis™ and ProteoSol™ are proprietary INTABIOTECH / ND Pharma & Biotech technology and brand designations. Product specifications, regulatory status and performance claims must be confirmed against the current controlled dossier, jurisdiction and lot-specific documentation before commercial use by third parties in different countries and territories. No description in this article grants access to or a licence over confidential manufacturing know-how.

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